

2009-11-22 0425-1257PUS1_ST25 (2)
SEQUENCE LISTING

<110> MACHIDA, Kazuhiro et al.
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<141> 2006-05-01
<150> JP 2003-396828
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<212> PRT

<213> Streptomyces sp.

<400> 6

Met Arg Ile Ala Ile Asp Thr Asp Arg Cys Ile Gly Ala Gly Gln Cys
 1 5 10 15

Ala Leu Thr Ala Pro Gly Gly Phe Thr Gln Asp Asp Asp Gly Phe Ser
 20 25 30

Ala Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly Asp Pro Leu Val Arg
 35 40 45

Glu Ala Ala Arg Ala Cys Pro Val Gln Ala Ile Ala Val Thr Asp Asp
 50 55 60

<210> 7

<211> 1860

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Sequence: nucleotide sequence with coding region derived from an unknown source

<220>

<221> CDS

<222> (172)..(1383)

<220>

<221> CDS

<222> (1399)..(1593)

<400> 7

cgggggatcgt acgccgtacc gtttcggggc aaccgaatta cgatgcggaa tggatggttc 60

ccagccagat cccgaggta gccgatctgg ccgaacttga tgtctgtcac tggatgcctc 120

gggcatctaa tgaagatcgg cagcacgcat ctttcgtctg cgaggtctcc c atg aca 177

Met Thr

gac acg aca gac ctg acc gag ctg tca gat ccc gtc tcc ttc ccc cag Asp Thr 5 Thr Asp Leu Thr Glu Leu Ser Asp Pro Val Ser Phe Pro Gln	225
gac cgg agc tgc ccc tac cac ccg ccc acc ggg tac gac ccg ctg cgc Asp Arg 20 Ser Cys Pro Tyr His 25 Pro Pro Thr Gly Tyr 30 Asp Pro Leu Arg	273
acc gaa cgg ccg ccc gcc cgc atc ccg ctc tac gac ggc cgc ccc gcc Thr 35 Glu Arg Pro Pro Ala 40 Arg Ile Arg Leu Tyr 45 Asp Gly Arg Pro Ala 50	321
tgg ctc gtc acc ggc cac gcc gtc gcc cgt gac ctg ctg gtc gac ccc Trp Leu Val Thr 55 His Ala Val Ala 60 Asp Asp Leu Leu Val 65 Asp Pro	369
cgc ctg tcc acg gac cgc acc cgc tgc ggc ttc ccg gcc aca act ccc Arg Leu Ser Thr 70 Asp Arg Thr Arg Ser 75 Gly Phe Pro Ala Thr 80 Thr Pro	417
cgc ttc gcc ggc gtc cgc gac ccg aag ccg ggc ctc ctc ggc gtc gac Arg Phe 85 Ala Ala Val Arg Asp Arg Lys Pro Ala Leu Leu Gly Val Asp	465
gac ccc aag cac cgc acc cag ctg tgg atg atg atc ccg agc ttc acc Asp Pro 100 Lys His Arg Thr 105 Gln Arg Trp Met Met Ile 110 Pro Ser Phe Thr	513
ctc agg cgc gcc acc gag ctg agg ccg cgc atc cag gag atc gtc gac Leu Arg Arg Ala Thr 120 Glu Leu Arg Pro Arg Ile 125 Gln Glu Ile Val Asp 130	561
gaa ctg ctg gac gtg atg atc gcc cag gga ccc ccg gcc gac ctg gtg Glu Leu Leu Asp Val 135 Met Ile Ala Gln Gly 140 Pro Pro Ala Asp 145 Leu Val	609
cgt tcc ttc gcg ctg ccg gtg ccg tcc atg gtg atc tgc gcc ctg ctc Arg Ser Phe Ala 150 Leu Pro Val 155 Met Val Ile Cys Ala 160 Leu Leu	657
ggc gtg ccc tac gcc gac cac gag ttc ttc gag gac cag tcc agg cgg Gly Val 165 Tyr Ala Asp His Glu 170 Phe Phe Glu Asp 175 Ser Arg Arg	705
ctg ctg cgc gga ccg gcg gcc gag gac acg cag gac gcc ccg gac cgg Leu Leu 180 Arg Gly Pro Ala 185 Glu Asp Thr Gln Asp 190 Ala Arg Asp Arg	753
ctc gcc gcg tac ctg gag gac ctg atc gac gag aag ccg cgc cgg ccc Leu Ala 195 Ala Tyr Leu Glu 200 Asp Leu Ile Asp 205 Lys Arg Arg Arg Pro 210	801
ggt gac ggc ctg ctg gac gaa ctc gtc cag cag cgt ctg aac gaa ggc Gly Asp Gly Leu 215 Asp Glu 220 Gln Gln Arg Leu Asn 225 Glu Gly	849
gag ctc gac ccg gag gaa ctg acc gcg ctg gcg atg atc ctg ctg gtc Glu Leu Asp Arg Glu 230 Glu Leu Thr 235 Leu Ala Met Ile Leu Leu Val	897
gcg ggc cac gag acc acc gcc aac atg atc tcc ctg ggc acc tac acg	945

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Ala	Gly	His	Glu	Thr	Thr	Ala	Asn	Met	Ile	Ser	Leu	Gly	Thr	Tyr	Thr	
		245					250					255				
ctc	ctg	ctg	cac	ccc	gaa	cgg	ctg	acc	gag	ctg	cgc	gcc	gac	ccc	gcg	993
Leu	Leu	Leu	His	Pro	Glu	Leu	Thr	Thr	Glu	Leu	Arg	Ala	Asp	Pro	Ala	
		260				265					270					
ctg	ctg	ccg	gcc	gcc	gtc	gag	gaa	ctg	atg	cgg	atg	ctg	tcc	atc	gcg	1041
Leu	Leu	Pro	Ala	Ala	Val	Glu	Glu	Leu	Met	Arg	Met	Leu	Ser	Ile	Ala	
		275			280					285					290	
gac	gga	ctg	ctg	cgg	cag	gcc	acc	gag	gac	atc	gag	atc	gcc	ggg	acc	1089
Asp	Gly	Leu	Leu	Arg	Gln	Ala	Thr	Glu	Asp	Ile	Glu	Ile	Ala	Gly	Thr	
				295					300					305		
acc	atc	agg	gcc	ggg	gac	ggc	gtg	gtc	ttc	tcc	acc	tct	gtc	atc	aac	1137
Thr	Ile	Arg	Ala	Gly	Asp	Gly	Val	Val	Phe	Ser	Thr	Ser	Val	Ile	Asn	
			310					315					320			
cgc	gac	gag	gac	gtc	tac	ccg	gcc	ccc	gac	acc	ctc	gac	ttc	cac	cgc	1185
Arg	Asp	Glu	Asp	Val	Tyr	Pro	Ala	Pro	Asp	Thr	Leu	Asp	Phe	His	Arg	
		325					330					335				
tcg	acc	cgc	cac	cac	gtc	gcc	ttc	ggt	ttc	gga	atc	cac	cag	tgc	ctc	1233
Ser	Thr	Arg	His	His	Val	Ala	Phe	Gly	Phe	Gly	Ile	His	Gln	Cys	Leu	
		340				345					350					
ggc	cag	aac	ctc	gcc	cgc	acc	gaa	ctg	gag	atc	gcc	ctg	cgc	acg	ctc	1281
Gly	Gln	Asn	Leu	Ala	Arg	Thr	Glu	Leu	Glu	Ile	Ala	Leu	Arg	Thr	Leu	
		355			360					365					370	
ctc	gaa	cgg	ctg	ccc	acg	ctc	cgg	ctc	gcc	gcc	cca	ccg	gag	gaa	atc	1329
Leu	Glu	Arg	Leu	Pro	Thr	Leu	Arg	Leu	Ala	Ala	Pro	Pro	Glu	Glu	Ile	
				375					380					385		
ccc	ttc	aaa	ccc	ggc	gac	acc	atc	cag	ggg	atg	ctg	gaa	ctc	ccc	gtc	1377
Pro	Phe	Lys	Pro	Gly	Asp	Thr	Ile	Gln	Gly	Met	Leu	Glu	Leu	Pro	Val	
			390					395					400			
agc	tgg	taagaggctg	ccgtc	atg	cat	atc	gag	atc	gac	aag	gac	cgc	tgc			1428
Ser	Trp			Met	His	Ile	Glu	Ile	Asp	Lys	Asp	Arg	Cys			
				405					410							
atc	ggc	gcc	gga	cag	tgc	gcc	ctg	acc	gcc	ccg	ggt	gtg	ttc	acc	cag	1476
Ile	Gly	Ala	Gly	Gln	Cys	Ala	Leu	Thr	Ala	Pro	Gly	Val	Phe	Thr	Gln	
		415			420				425						430	
gac	gac	gac	ggc	ttc	agt	gac	ctg	ttg	ccc	ggc	cgg	gag	gac	ggc	gcc	1524
Asp	Asp	Asp	Gly	Phe	Ser	Asp	Leu	Leu	Pro	Gly	Arg	Glu	Asp	Gly	Ala	
			435						440					445		
ggc	gac	ccg	atg	gtc	cgg	gag	gcc	agg	gcc	tgc	ccc	gtg	agt	gcc		1572
Gly	Asp	Pro	Met	Val	Arg	Glu	Ala	Ala	Arg	Ala	Cys	Pro	Val	Ser	Ala	
			450					455					460			
atc	acg	ctg	tcc	gag	gac	ggg	tagggggccg	agccgcgcgcg	cccgcgggtc							1623
Ile	Thr	Leu	Ser	Glu	Asp	Gly										
				465												
cgctgccgcg	gcgccgtgcc	gacgcggcgg	ccggccggcc	cgctccgggtgc	ccgtcgcgtc											1683
gccccgtggc	ccccggcgcg	gctgattgac	taggggtccc	gggtgagcga	acaggcccgag											1743

aagccctccg gggcgccgcc cgcgaaagac accgggacgg cgcccgga accccttcct 1803
ctacgtcgtc gtctgcgcgc ccggcatcgc cgaaggcgtc agcaagctga tcaccgc 1860

<210> 8
<211> 404
<212> PRT
<213> Unknown

<220>
<223> Derived from an unknown source

<400> 8

Met Thr Asp Thr Thr Asp Leu Thr Glu Leu Ser Asp Pro Val Ser Phe
1 5 10 15

Pro Gln Asp Arg Ser Cys Pro Tyr His Pro Pro Thr Gly Tyr Asp Pro
20 25 30

Leu Arg Thr Glu Arg Pro Pro Ala Arg Ile Arg Leu Tyr Asp Gly Arg
35 40 45

Pro Ala Trp Leu Val Thr Gly His Ala Val Ala Arg Asp Leu Leu Val
50 55 60

Asp Pro Arg Leu Ser Thr Asp Arg Thr Arg Ser Gly Phe Pro Ala Thr
65 70 75 80

Thr Pro Arg Phe Ala Ala Val Arg Asp Arg Lys Pro Ala Leu Leu Gly
85 90 95

Val Asp Asp Pro Lys His Arg Thr Gln Arg Trp Met Met Ile Pro Ser
100 105 110

Phe Thr Leu Arg Arg Ala Thr Glu Leu Arg Pro Arg Ile Gln Glu Ile
115 120 125

Val Asp Glu Leu Leu Asp Val Met Ile Ala Gln Gly Pro Pro Ala Asp
130 135 140

Leu Val Arg Ser Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys Ala
145 150 155 160

Leu Leu Gly Val Pro Tyr Ala Asp His Glu Phe Phe Glu Asp Gln Ser
165 170 175

Arg Arg Leu Leu Arg Gly Pro Ala Ala Glu Asp Thr Gln Asp Ala Arg
180 185 190

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Asp Arg Leu Ala Ala Tyr Leu Glu Asp Leu Ile Asp Glu Lys Arg Arg
195 200 205

Arg Pro Gly Asp Gly Leu Leu Asp Glu Leu Val Gln Gln Arg Leu Asn
210 215 220

Glu Gly Glu Leu Asp Arg Glu Glu Leu Thr Ala Leu Ala Met Ile Leu
225 230 235 240

Leu Val Ala Gly His Glu Thr Thr Ala Asn Met Ile Ser Leu Gly Thr
245 250 255

Tyr Thr Leu Leu Leu His Pro Glu Arg Leu Thr Glu Leu Arg Ala Asp
260 265 270

Pro Ala Leu Leu Pro Ala Ala Val Glu Glu Leu Met Arg Met Leu Ser
275 280 285

Ile Ala Asp Gly Leu Leu Arg Gln Ala Thr Glu Asp Ile Glu Ile Ala
290 295 300

Gly Thr Thr Ile Arg Ala Gly Asp Gly Val Val Phe Ser Thr Ser Val
305 310 315 320

Ile Asn Arg Asp Glu Asp Val Tyr Pro Ala Pro Asp Thr Leu Asp Phe
325 330 335

His Arg Ser Thr Arg His His Val Ala Phe Gly Phe Gly Ile His Gln
340 345 350

Cys Leu Gly Gln Asn Leu Ala Arg Thr Glu Leu Glu Ile Ala Leu Arg
355 360 365

Thr Leu Leu Glu Arg Leu Pro Thr Leu Arg Leu Ala Ala Pro Pro Glu
370 375 380

Glu Ile Pro Phe Lys Pro Gly Asp Thr Ile Gln Gly Met Leu Glu Leu
385 390 395 400

Pro Val Ser Trp

<210> 9
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Derived from an unknown source

<400> 9

Met His Ile Glu Ile Asp Lys Asp Arg Cys Ile Gly Ala Gly Gln Cys
1 5 10 15

Ala Leu Thr Ala Pro Gly Val Phe Thr Gln Asp Asp Asp Gly Phe Ser
20 25 30

Asp Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly Asp Pro Met Val Arg
35 40 45

Glu Ala Ala Arg Ala Cys Pro Val Ser Ala Ile Thr Leu Ser Glu Asp
50 55 60

Gly
65

<210> 10

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : 5Dm-3F Primer

<400> 10

ttcgscctsc csgtccctsc satggtsat

29

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : 5Dm-3R Primer

<400> 11

gttgatsays gasgtsgaga a

21

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : 6PIN-2F Primer

<400> 12

gctgcgcttg gccctggagg acatcgagat

30

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 6PIN-2R Primer

<400> 13
 ctgttcctcg aagaactcgt ggtcggcgta 30

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : DM-NdeF Primer

<400> 14
 gccccatat gacggaactg acggacatca 30

<210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : DM-SpeR Primer

<400> 15
 gggccactag tcagccggcc ggttcggtca 30

<210> 16
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : DM-BglF Primer

<400> 16
 cgcatagatc ttcacccgag cgggtgatca 30

<210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : DM-BglR Primer

<400> 17
 tcccagatc ttgaaggcc gcgtaccgt 30

<210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 5D-1R Primer

<400> 18
 aggtgccag cgagatcatg tt 22

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 7PIN-2F Primer

<400> 19
 ccatgatcct gctgggtgcc ggccatgaga 30

<210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 07-NdeF Primer

<400> 20
 gccccatag accgaagcca tccccactt 30

<210> 21
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 07-SpeR Primer

<400> 21
 gccactagtg ctaatcgctg gtgaccgcaa 30

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 5Dm-2R Primer

<400> 22
 ctggatsgtg tcscsggyt t 21

<210> 23
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : 5PIN-2F Primer

<400> 23
 cggaatccac cagtgcctcg gccagaacct 30

<210> 24
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : tpm-NdeF Primer

<400> 24
 ggccccatat gacagacacg acagacctga

30

<210> 25
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : tpm-SpeR Primer

<400> 25
 gcgcgactag tccccctacc cgtcctcgga

30